```
NGCGGTCAAGCTTGAGGCGTCATCTGGCTGCGCCTAGTGGGCCGTTGCCTTACAGTTGCTGAGAGGAGGTGAGAGGCGG

                                                                  M  K          2
GGGCGCTAGGGCCGAGATCATGTCTGACTGGGAGAGGTTTCCTTGGCAGCAGAGGACGCTAGGTTTGGG ATG AAA      6

 E  A  G  Q  M  Q  N  L  E  S  A  R  A  G  R  S  V  S  T  Q                  22
GAA GCT GGG CAG ATG CAA AAT CTG GAG AGC GCG AGG GCC GGG CGG TCA GTC AGC ACC CAG    66

 T  G  S  M  T  G  Q  I  P  R  L  S  K  V  N  L  F  T  L  L                  42
ACT GGC AGC ATG ACC GGT CAG ATA CCA AGG CTT TCT AAA GTC AAC CTT TTC ACT CTG CTC   126

 S  L  W  M  E  L  F  P  A  E  A  Q  R  Q  K  S  Q  K  N  E                  62
AGC CTC TGG ATG GAG CTC TTT CCA GCA GAA GCC CAG CGG CAA AAA TCT CAG AAA AAT GAA   186

 E  G  K  H  G  P  L  G  D  N  E  E  R  T  R  V  S  T  D  K                  82
GAG GGA AAG CAT GGA CCC TTA GGA GAT AAT GAA GAG AGG ACC AGA GTA TCT ACT GAC AAA   246

 R  Q  V  K  R  T  G  L  V  V  V  K  N  M  K  I  V  G  L  H                 102
AGA CAG GTA AAG AGA ACT GGT CTT GTG GTG GTG AAA AAC ATG AAA ATT GTT GGT CTC CAC   306

 C  S  S  E  D  L  H  A  G  Q  I  A  L  I  K  H  G  S  R  L                 122
TGT TCT AGT GAA GAT TTA CAT GCC GGG CAG ATT GCT CTT ATT AAA CAT GGG TCA AGG CTG   366

 K  N  C  D  L  Y  F  S  R  K  P  C  S  A  C  L  K  M  I  V                 142
AAA AAC TGT GAT CTT TAT TTT TCC AGA AAA CCA TGT TCT GCT TGT TTG AAA ATG ATT GTA   426

 N  A  G  V  N  R  I  S  Y  W  P  A  D  P  E  I  S  L  L  T                 162
AAT GCT GGA GTT AAC CGA ATT TCA TAC TGG CCT GCT GAT CCA GAA ATA AGT TTG CTT ACG   486

 E  A  S  S  S  E  D  A  K  L  D  A  K  A  V  E  R  L  K  S                 182
GAG GCT TCT AGT TCT GAA GAT GCA AAG TTA GAT GCC AAA GCA GTG GAA AGA TTG AAG TCA   546

 N  S  R  A  H  V  C  V  L  L  Q  P  L  V  C  Y  M  V  Q  F                 202
AAC AGT CGG GCC CAT GTG TGT GTC TTA CTT CAA CCT TTG GTG TGT TAT ATG GTG CAG TTT   606

 V  E  E  T  S  Y  K  C  D  F  I  Q  K  I  T  K  T  L  P  D                 222
GTA GAG GAG ACC TCT TAC AAA TGT GAC TTT ATT CAA AAA ATT ACA AAA ACA TTG CCG GAT   666

 A  N  T  D  F  Y  Y  E  C  K  Q  E  R  I  K  E  Y  E  M  L                 242
GCT AAC ACT GAC TTT TAT TAT GAA TGT AAA CAA GAA AGA ATA AAA GAA TAT GAA ATG TTA   726

 F  L  V  S  N  E  E  M  H  K  Q  I  L  M  T  I  G  L  E  N                 262
TTT TTG GTT TCA AAT GAA GAA ATG CAT AAG CAA ATA CTG ATG ACT ATA GGT TTG GAG AAC   786

 L  C  E  N  P  Y  F  S  N  L  R  Q  N  M  K  D  L  I  L  L                 282
CTG TGT GAA AAT CCA TAC TTT AGC AAT CTA AGG CAA AAC ATG AAA GAC CTT ATC CTA CTT   846

 L  A  T  V  A  S  S  V  P  N  F  K  H  F  G  F  Y  R  S  N                 302
TTG GCC ACA GTA GCT TCC AGT GTG CCG AAC TTT AAA CAC TTC GGA TTT TAC CGT AGC AAT   906

 P  E  Q  I  N  E  I  H  N  Q  S  L  P  Q  E  I  A  R  H  C                 322
CCA GAA CAG ATT AAT GAA ATT CAC AAT CAA AGT TTG CCA CAG GAA ATT GCA AGG CAC TGC   966

 M  V  Q  A  R  L  L  A  Y  R  T  G  E  L  H  R  S  *                       340
ATG GTT CAG GCC AGG TTA TTG GCA TAT CGA ACT GGT GAG TTA CAT AGA TCG TAA         1020

ATTGGGGCTGATTGGTTGGGTTGTATTTGTCTCTGAAGTGTTCGTCTCATTTATGGTAGAGTTCATTTACTCATAGTTA
```

FIG. 1A.

CTTAAGTTTTGCTGTTCATACAATATAGAGAAGTTAGTGAGACCCTTGAGTAGACAACTCTTTCTCCCAGCAGTTTTGG

GATTCCTTGTAGCCTTATATTCAGTACCACATTTCTACATCAGGCCCTCATTAATCTAGGCCCTTCTTTCTGCTTCTTG

CTTTTATGATTTCACTGKTCCTTGAGCCCTCCACTAAAGGTAGGACAAGAAGAGAAAGGAGAGGCCCAGTGCAGTGGTT

CATGCCTGTAATTGCAACACTTTAGAAGGCTGADACAGGAGGATCGCTTGAGCTCAGGAGTTCAAGACCAGCGTGGGCA

ACATAGCAAGACCTCGACTCTA

FIG. 1B.

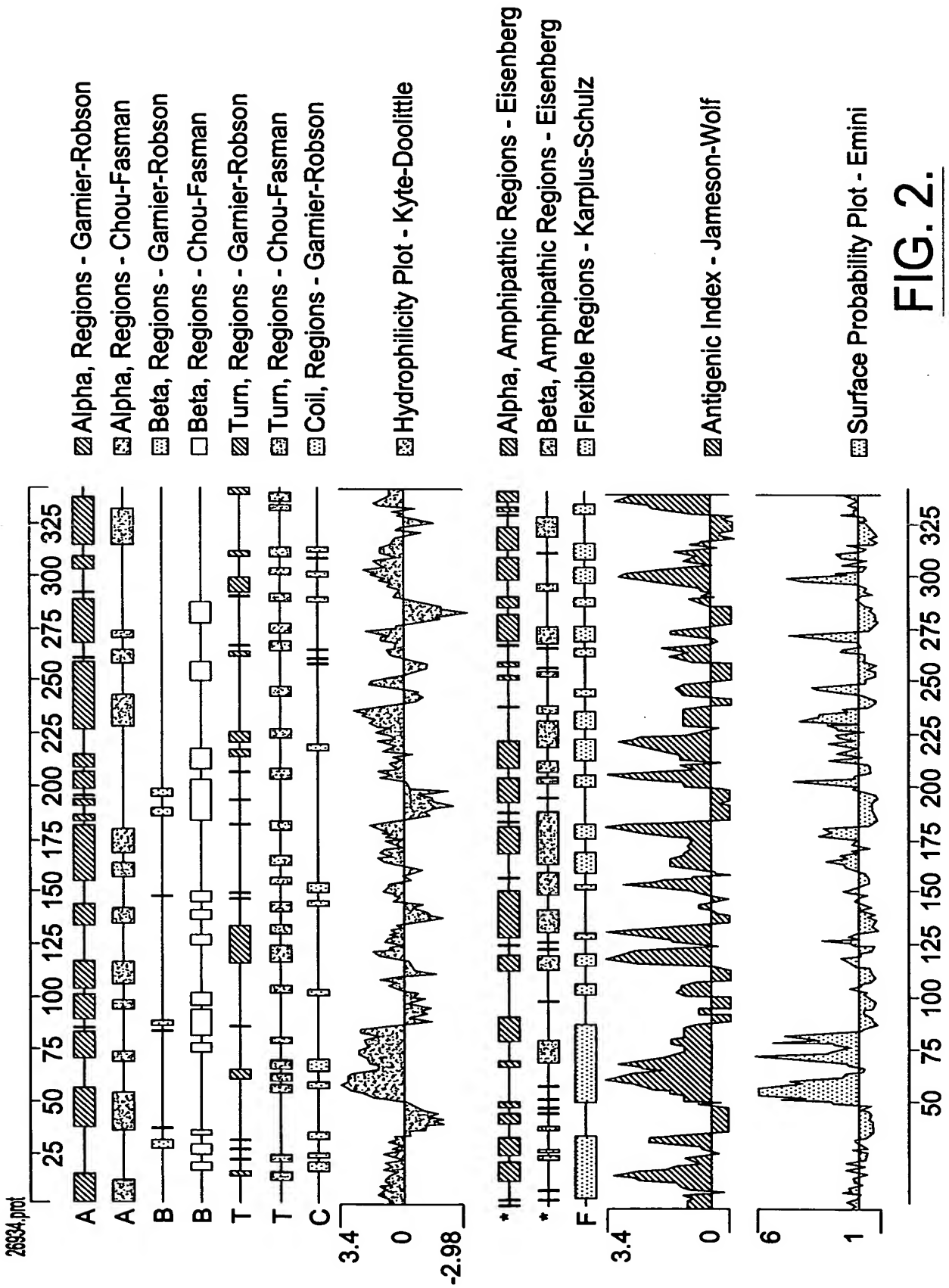

26934.pro
Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
Hydrophilicity Plot - Kyte-Doolittle
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
Flexible Regions - Karplus-Schulz
Antigenic Index - Jameson-Wolf
Surface Probability Plot - Emini
25 50 75 100 125 150 175 200 225 250 275 300 325
3.4
0
-2.98
6
1

FIG. 2.

Protein Family / Domain Matches, HMMer version 2

```
Searching for complete domains in PFAM
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
--------------------------------------------------------------------------
HMM file:                 /prod/ddm/seqanal/PFAM/pfam4.4/Pfam
Sequence file:            /tmp/orfanal.14420.aa
--------------------------------------------------------------------------
 Query:  26934
Scores for sequence family classification (score includes all domains):
Model        Description                                   Score    E-value  N
---------    -----------                                   ------   -------- ---
dCMP_cyt_deam Cytidine and deoxycytidylate deaminase        26.8    0.00052   1

Parsed for domains:
Model        Domain  seq-f seq-t    hmm-f hmm-t      score  E-value
---------    ------- ----- -----    ----- -----      ------ -------
dCMP_cyt_deam  1/1      80   149 . .     1   100 []   26.8  0.00052

Alignments of top-scoring domains:
dCMP_cyt_deam: domain 1 of 1, from 80 to 149: score 26.8, E = 0.00052
                   *->tpysgfpvGavivkdnGrifgvnseganyveGeqkkdptaHAEvnAI
                      t++ ++++   +v +n      ++  ++++e        +HA + A+
      26934    80    TDKRQVKRTGLVVVKN----MKIVGLHCSSE-------DLHAGQIAL 115

                   rkAvseryrdFkir1gger1egat1YvT1ePCgHyGRTpmCaqai iesgi
                   +K    +          r1++++1Y +  PC        C ++i+++g+
      26934   116 IK-H--G----------SRLKNCDLYFSRKPC------SACLKMIVNAGV 146

                   kkV<-*
                    ++
      26934   147 NRI    149
```

FIG. 3.

TO FIG. 4B.

FIG. 4A.

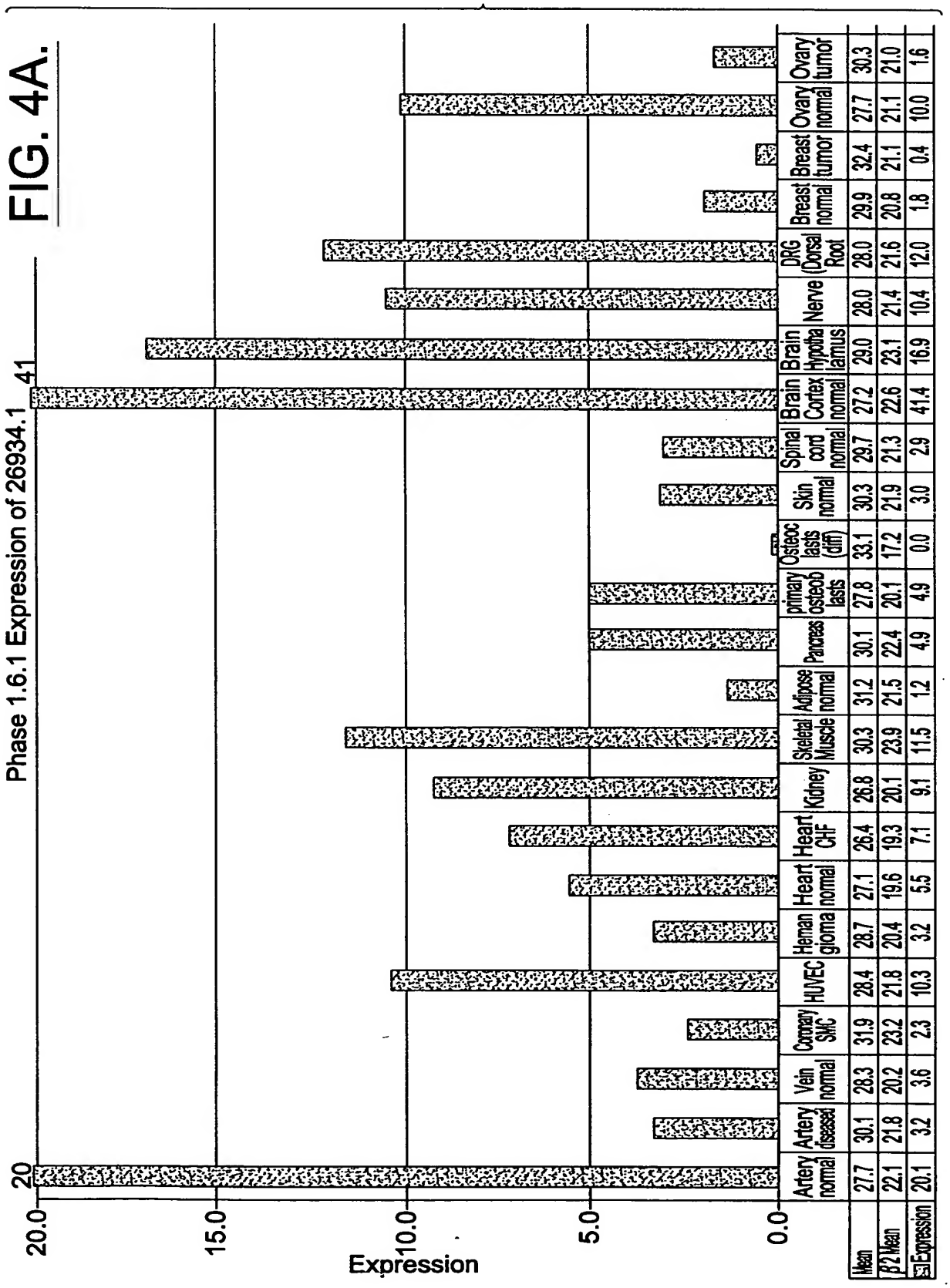
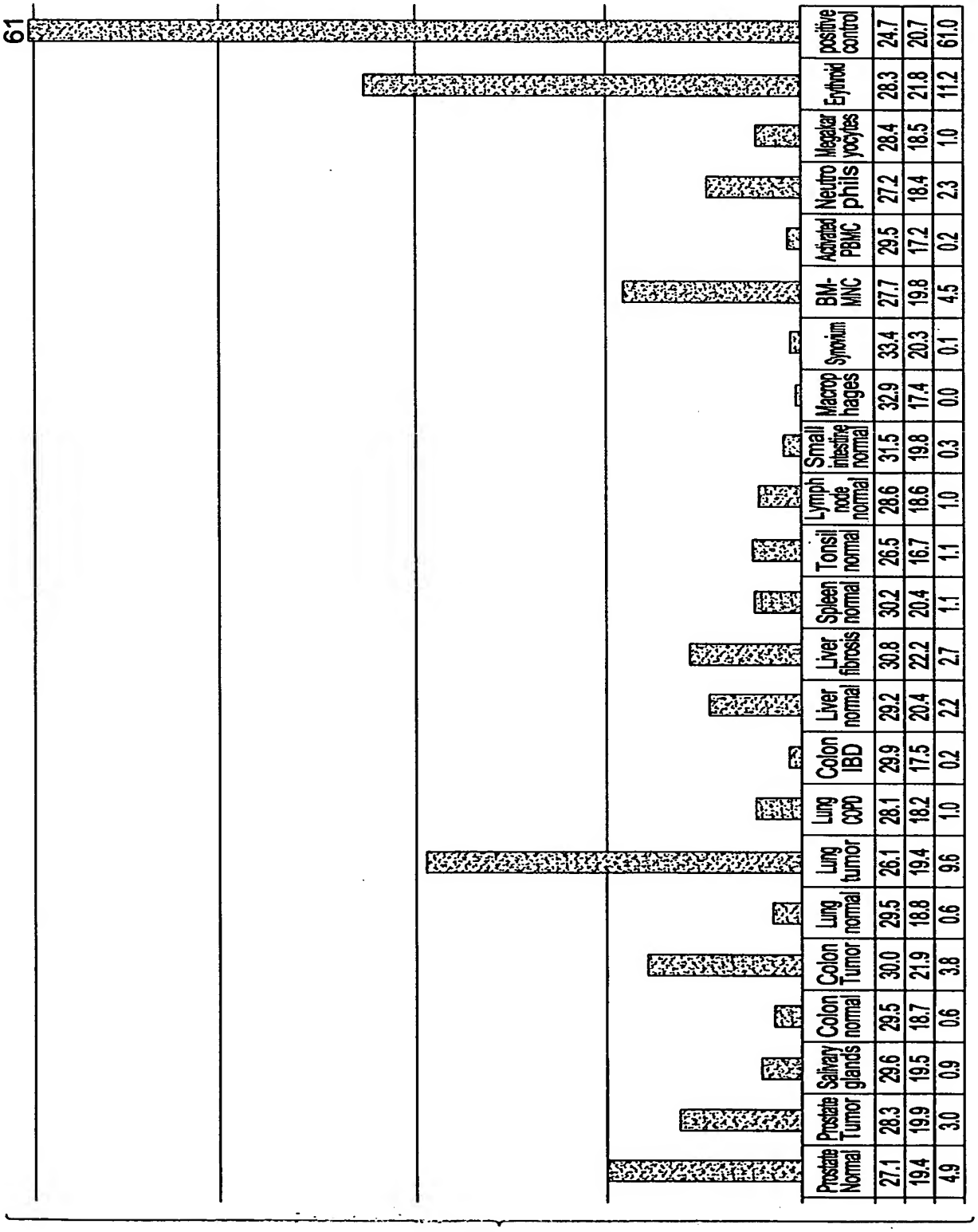


FIG. 4B.



FROM FIG. 4A.

FIG. 5A.

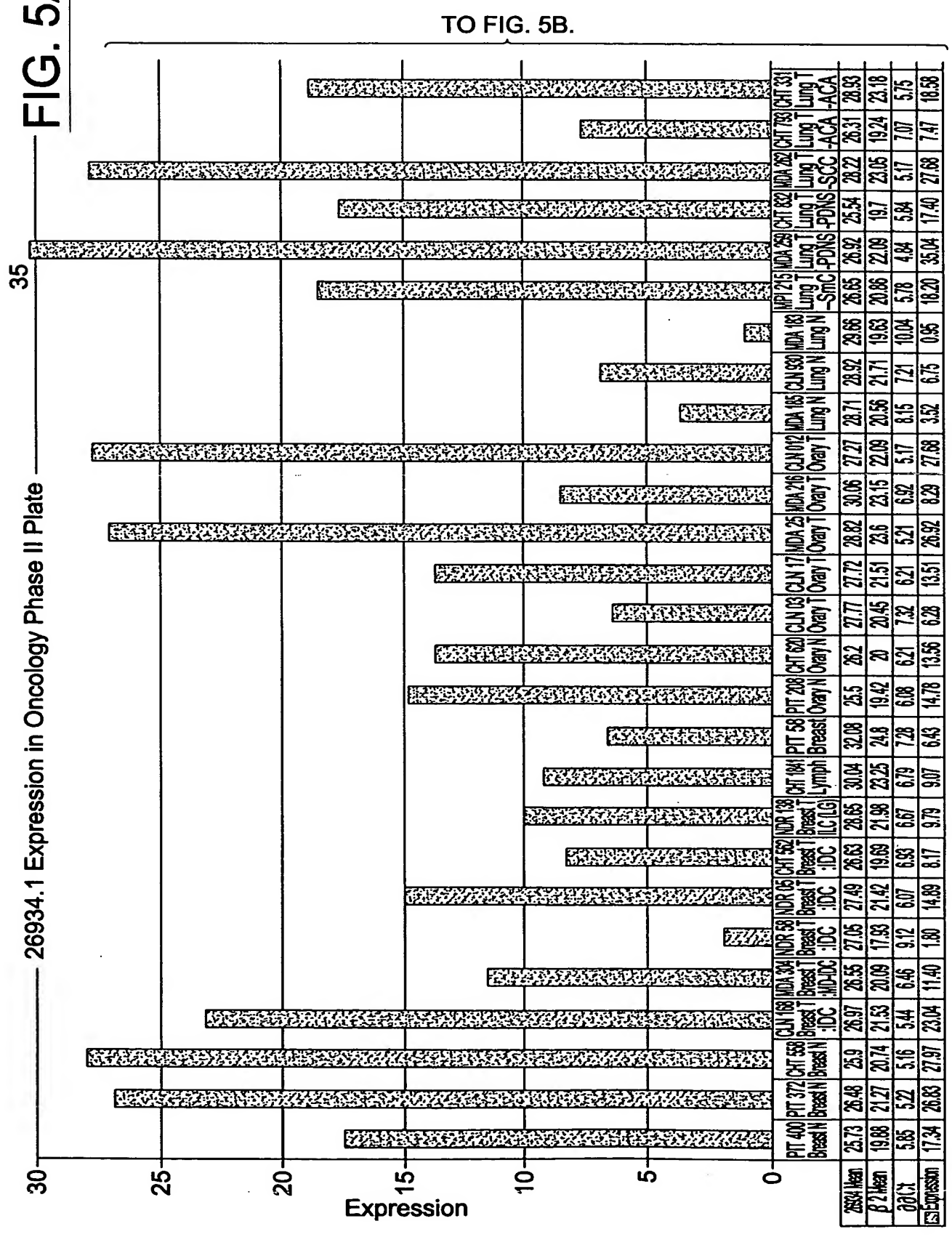
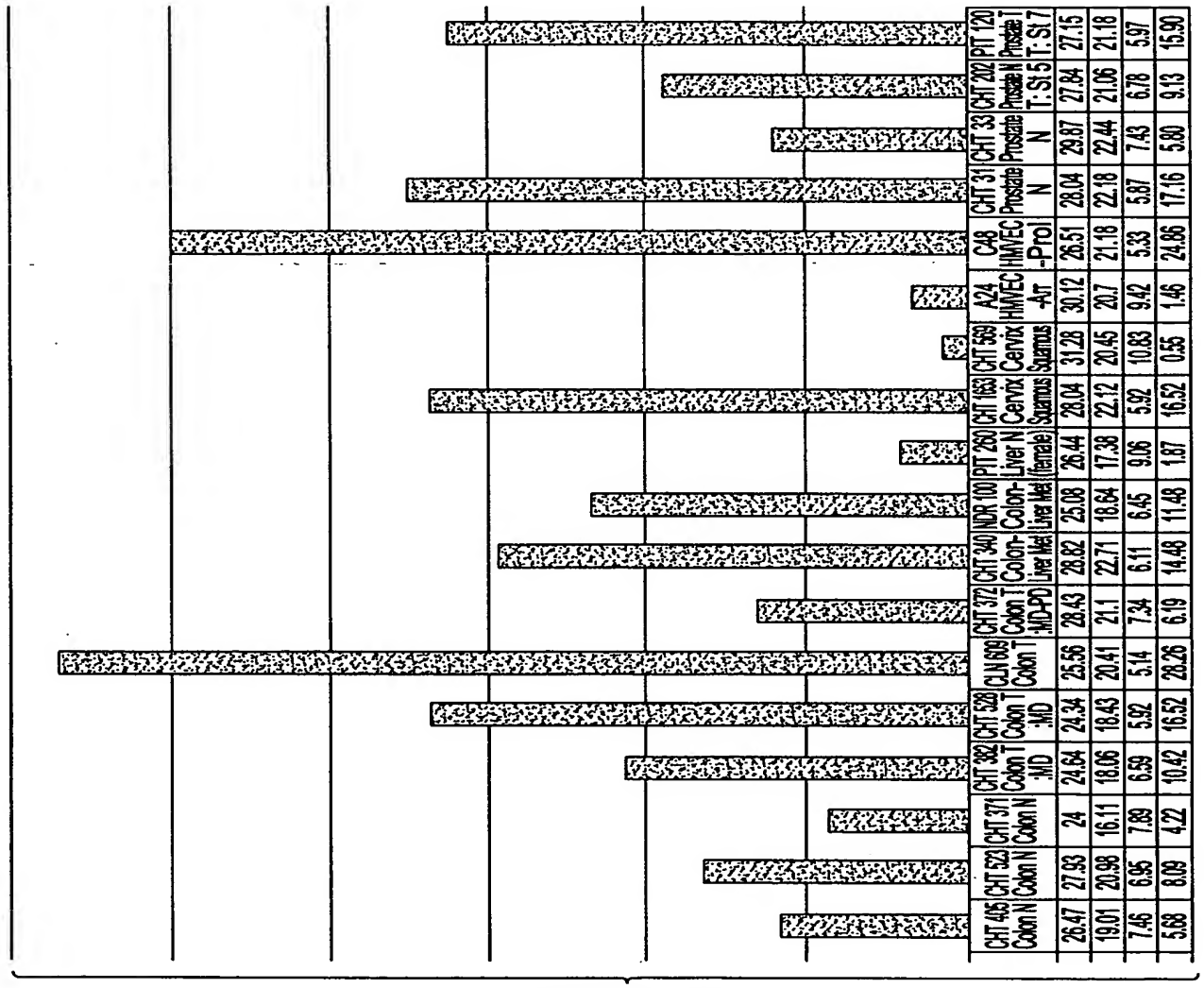

TO FIG. 5B.
26934.1 Expression in Oncology Phase II Plate
Expression
30
25
20
15
10
5
0
35
PIT 400 Breast N
PIT 372 Breast N
CHT 558 Breast N
CLN 168 Breast T :IDC
MDA 304 Breast T :MD-IDC
NDR 58 Breast T :IDC
NDR 05 Breast T :IDC
CHT 562 Breast T :IDC
NDR 139 Breast T :ILC (LG)
CHT 1941 Lymph
PIT 58 Breast
PIT 208 Ovary N
CHT 620 Ovary N
CLN 03 Ovary T
CLN 17 Ovary T
MDA 25 Ovary T
MDA 216 Ovary T
CLN 012 Ovary T
MDA 185 Lung N
CLN 930 Lung N
MDA 183 Lung N
MPI 215 Lung T -SmC
MDA 258 Lung T -PDNS
CHT 822 Lung T -PDNS
MDA 262 Lung T -SCC
CHT 783 Lung T -ACA
CHT 331 Lung T -ACA
26934 Mean
β 2 Mean
26934 Expression
25.73 19.88 5.85 17.34
26.48 21.27 5.22 26.83
25.9 20.74 5.16 27.97
26.97 21.53 5.44 23.04
26.55 20.09 6.46 11.40
27.05 17.93 9.12 1.80
27.49 21.42 6.07 14.89
26.63 19.69 6.93 8.17
28.65 21.98 6.67 9.79
30.04 23.25 6.79 9.07
32.08 24.8 7.28 6.43
25.5 19.42 6.08 14.78
26.2 20 6.21 13.56
27.77 20.45 7.32 6.28
27.72 21.51 6.21 13.51
28.82 23.6 5.21 26.92
30.06 23.15 6.92 8.29
27.27 22.09 5.17 27.68
28.71 20.56 8.15 3.52
28.92 21.71 7.21 6.75
29.66 19.63 10.04 0.95
26.65 20.86 5.78 18.20
26.92 22.09 4.84 35.04
25.54 19.7 5.84 17.40
28.22 23.05 5.17 27.68
26.31 19.24 7.07 7.47
28.93 23.18 5.75 18.58

FIG. 5B.



FROM FIG. 5A.

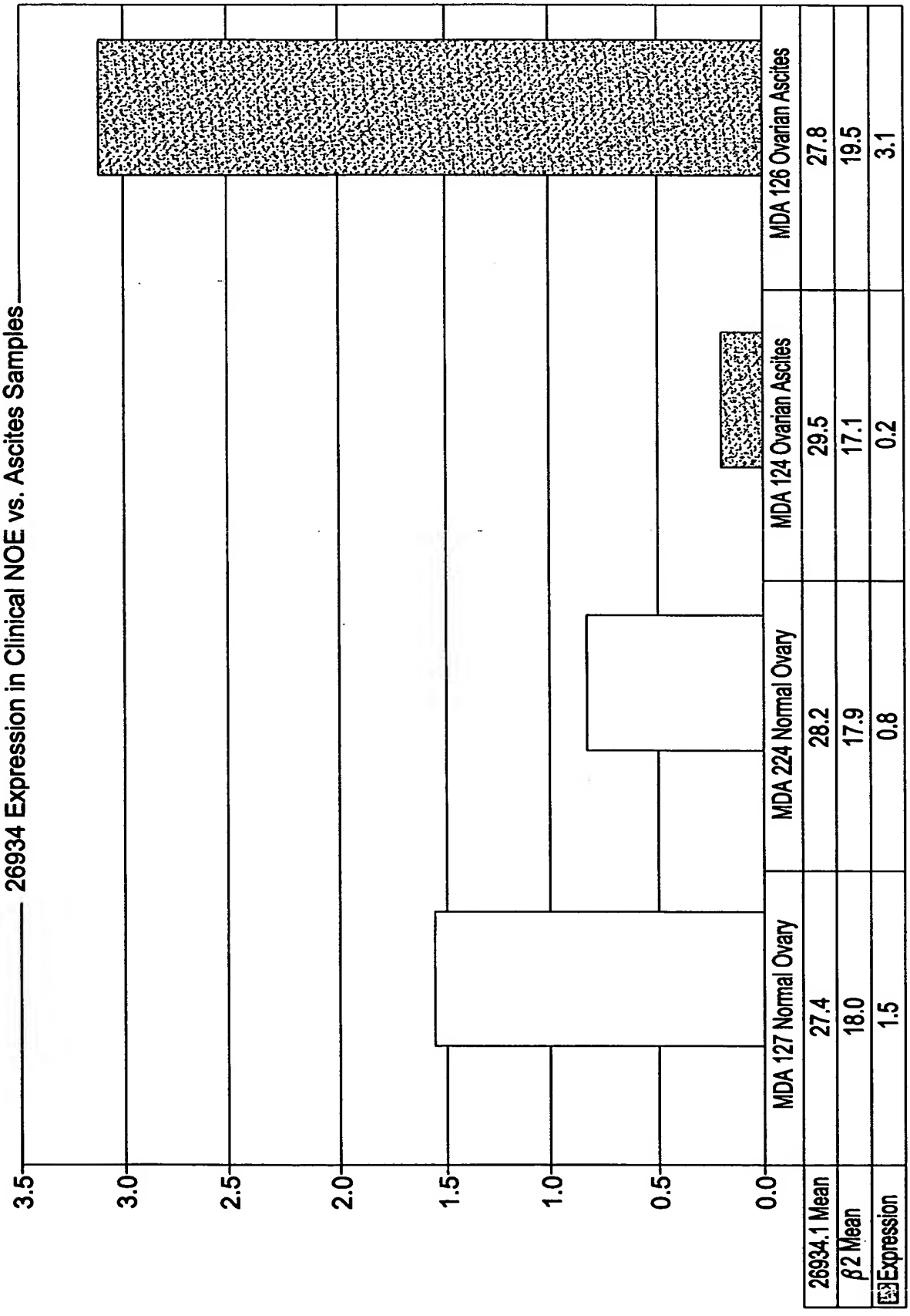

26934 Expression in Clinical NOE vs. Ascites Samples
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
MDA 127 Normal Ovary
MDA 224 Normal Ovary
MDA 124 Ovarian Ascites
MDA 126 Ovarian Ascites
26934.1 Mean
27.4
28.2
29.5
27.8
β2 Mean
18.0
17.9
17.1
19.5
Expression
1.5
0.8
0.2
3.1

FIG. 6.

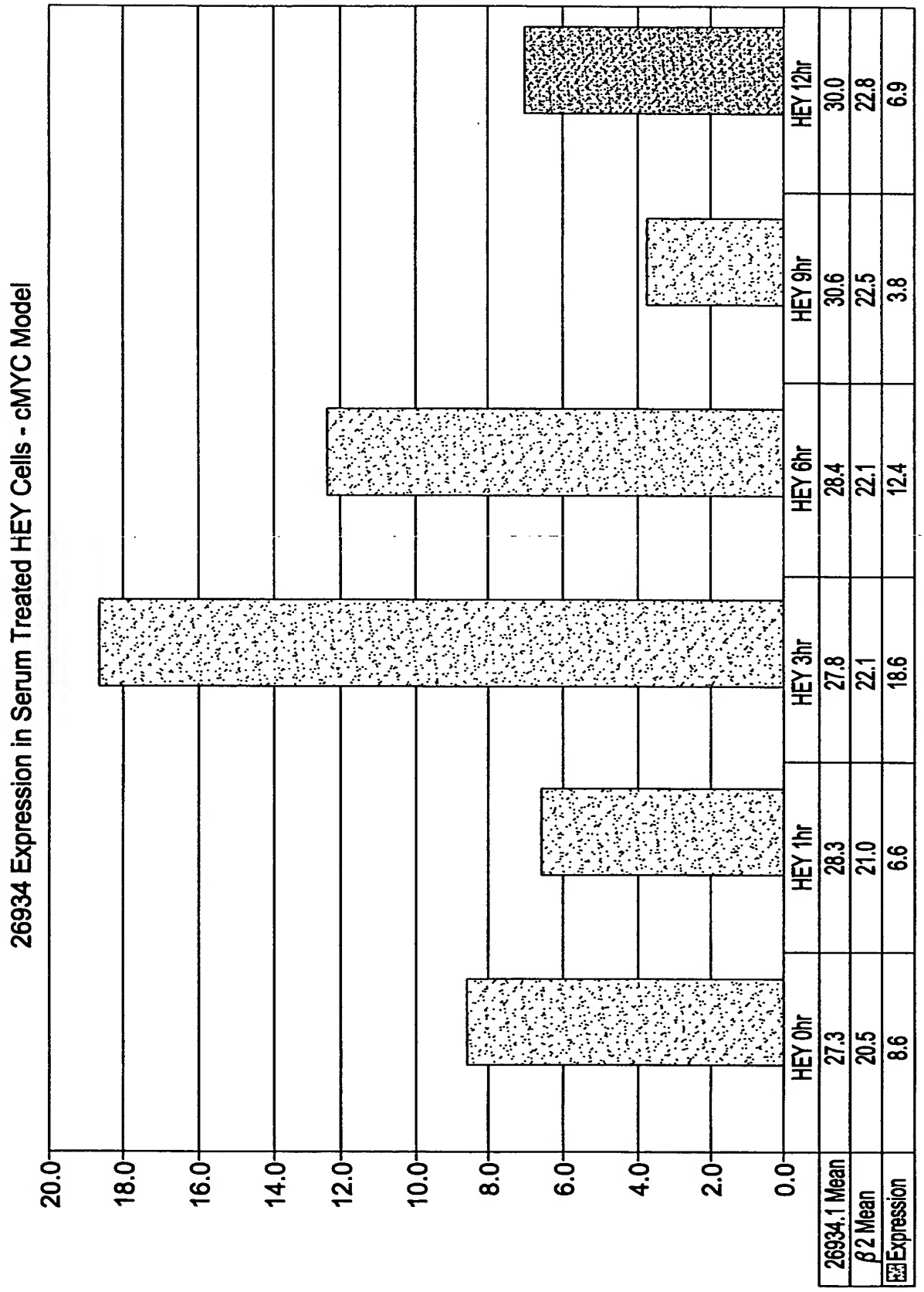

26934 Expression in Serum Treated HEY Cells - cMYC Model
20.0
18.0
16.0
14.0
12.0
10.0
8.0
6.0
4.0
2.0
0.0
HEY 0hr
HEY 1hr
HEY 3hr
HEY 6hr
HEY 9hr
HEY 12hr
26934.1 Mean
27.3
28.3
27.8
28.4
30.6
30.0
β2 Mean
20.5
21.0
22.1
22.1
22.5
22.8
Expression
8.6
6.6
18.6
12.4
3.8
6.9

FIG. 7.

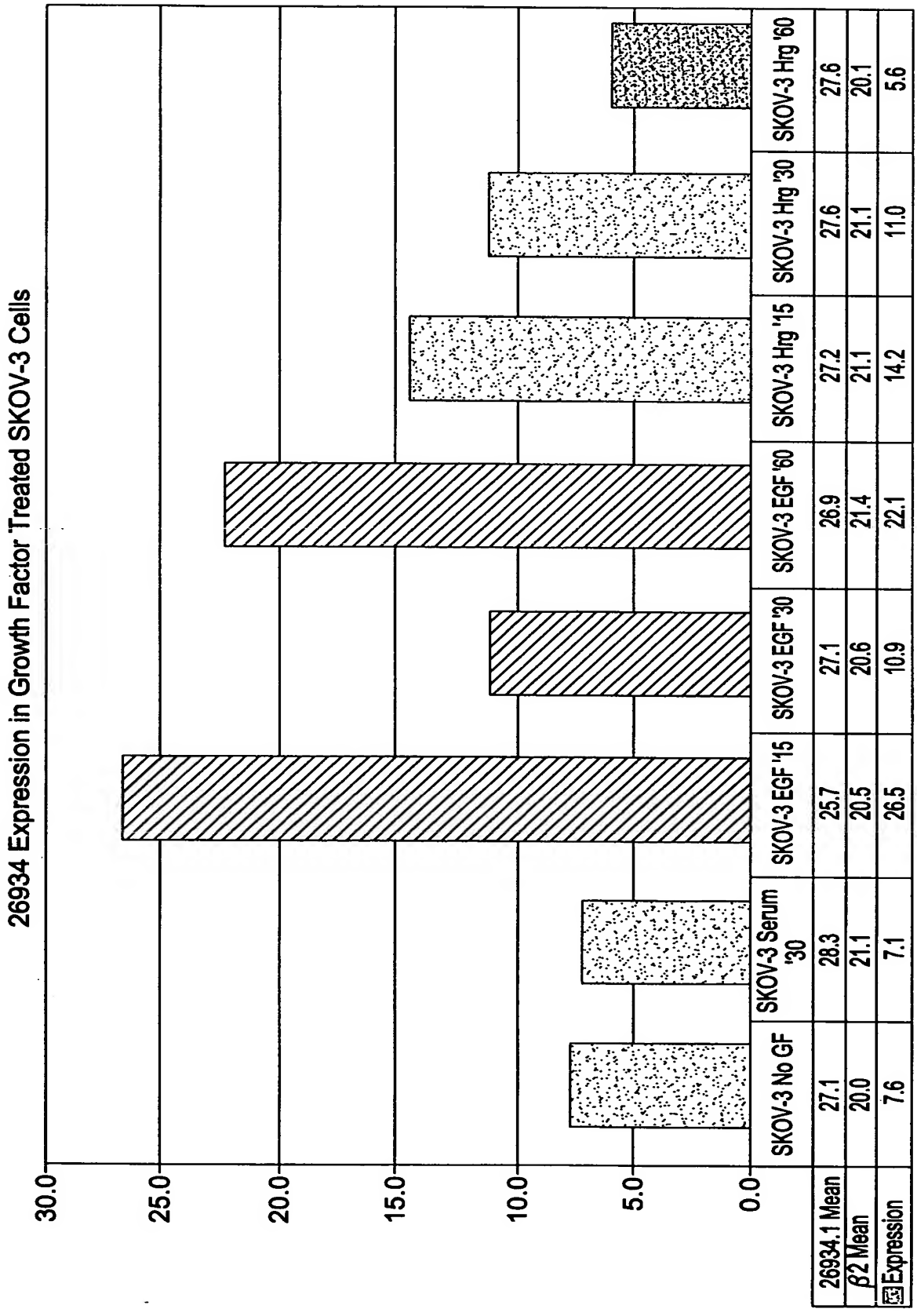

26934 Expression in Growth Factor Treated SKOV-3 Cells
30.0
25.0
20.0
15.0
10.0
5.0
0.0
SKOV-3 No GF
SKOV-3 Serum '30
SKOV-3 EGF '15
SKOV-3 EGF '30
SKOV-3 EGF '60
SKOV-3 Hrg '15
SKOV-3 Hrg '30
SKOV-3 Hrg '60
26934.1 Mean
27.1
28.3
25.7
27.1
26.9
27.2
27.6
27.6
β2 Mean
20.0
21.1
20.5
20.6
21.4
21.1
21.1
20.1
Expression
7.6
7.1
26.5
10.9
22.1
14.2
11.0
5.6

FIG. 8.

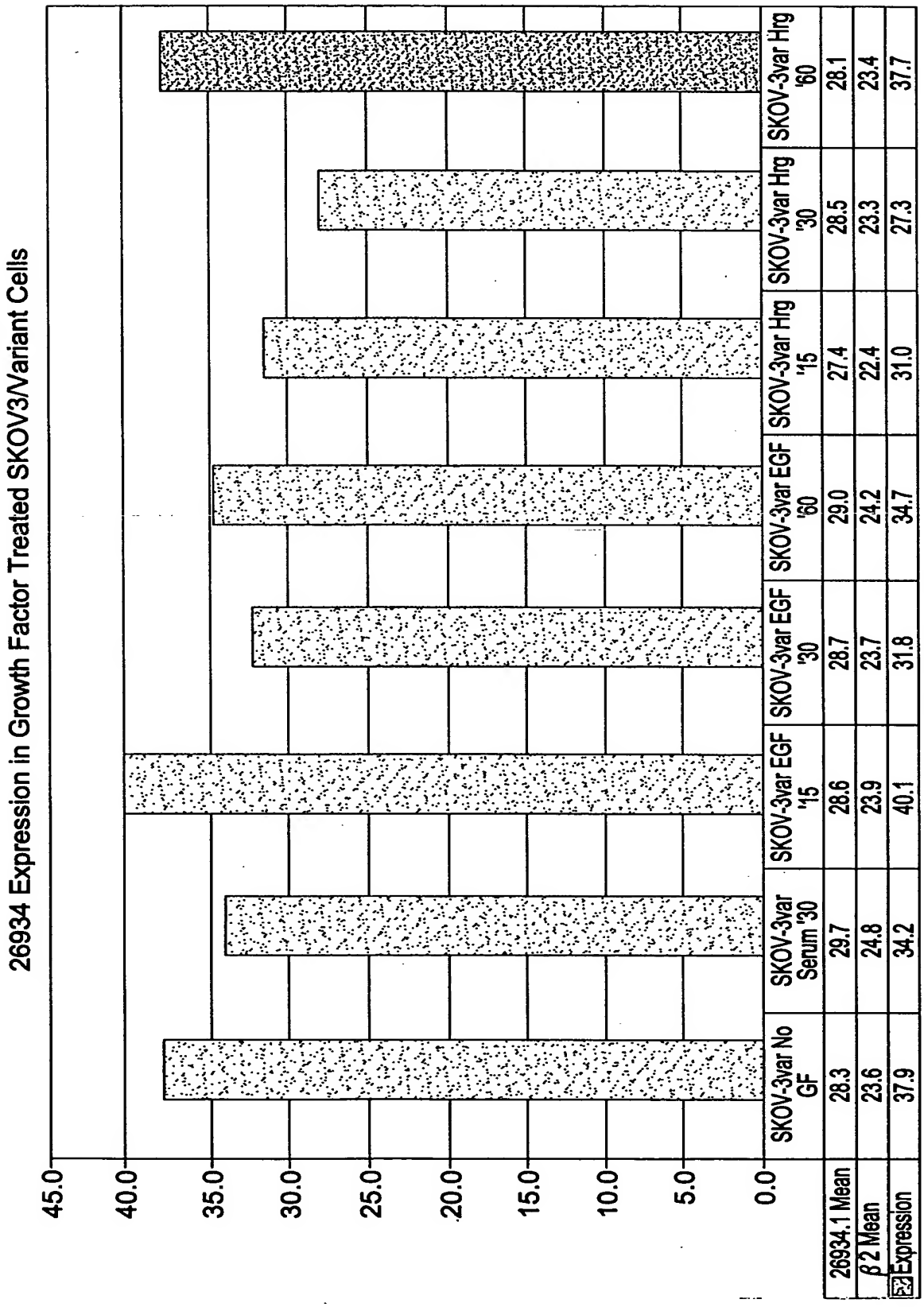

26934 Expression in Growth Factor Treated SKOV3/Variant Cells
45.0
40.0
35.0
30.0
25.0
20.0
15.0
10.0
5.0
0.0
SKOV-3var No GF
SKOV-3var Serum '30
SKOV-3var EGF '15
SKOV-3var EGF '30
SKOV-3var EGF '60
SKOV-3var Hrg '15
SKOV-3var Hrg '30
SKOV-3var Hrg '60
26934.1 Mean
28.3
29.7
28.6
28.7
29.0
27.4
28.5
28.1
β2 Mean
23.6
24.8
23.9
23.7
24.2
22.4
23.3
23.4
Expression
37.9
34.2
40.1
31.8
34.7
31.0
27.3
37.7

FIG. 9.

FIG. 10A.

TO FIG. 10B.

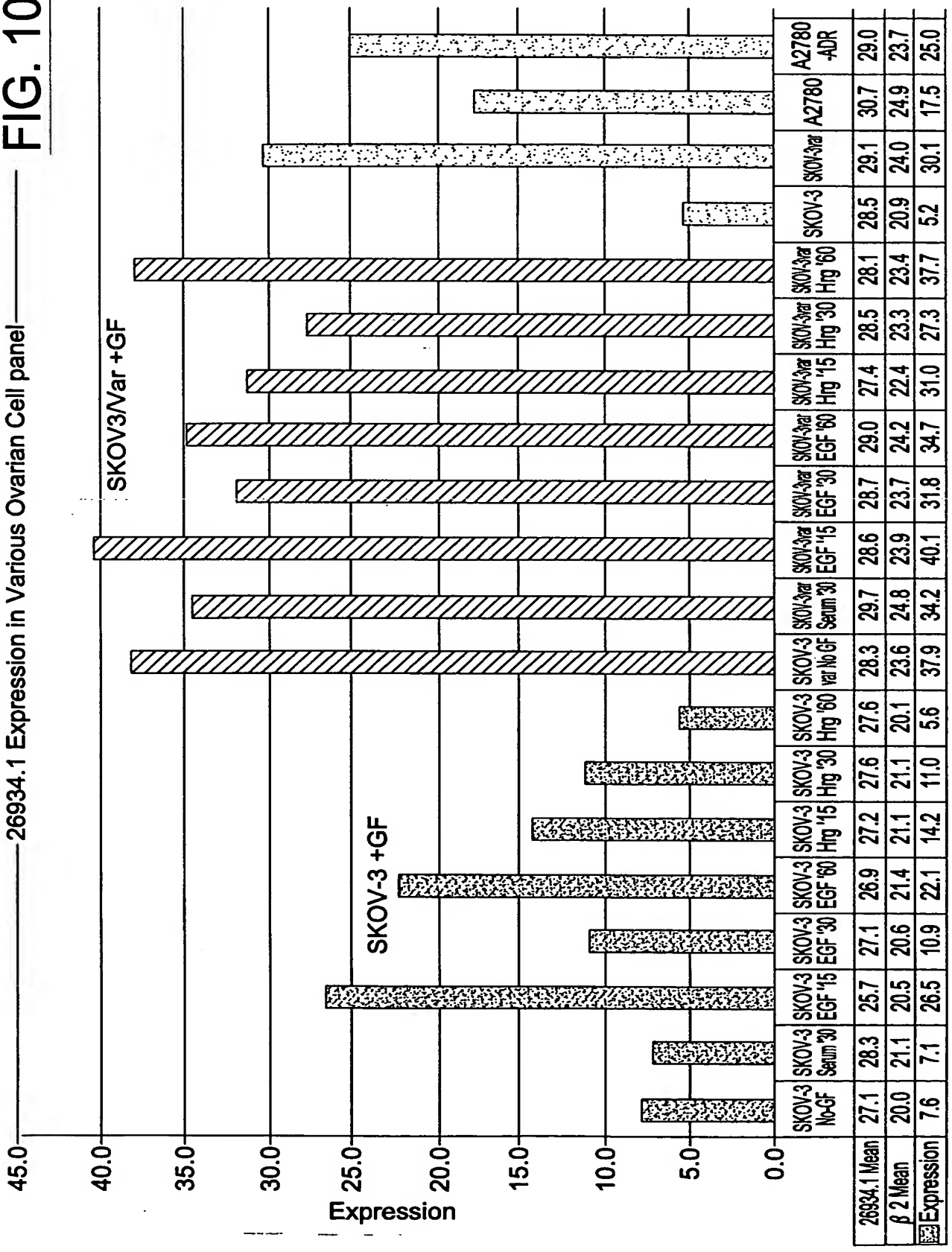
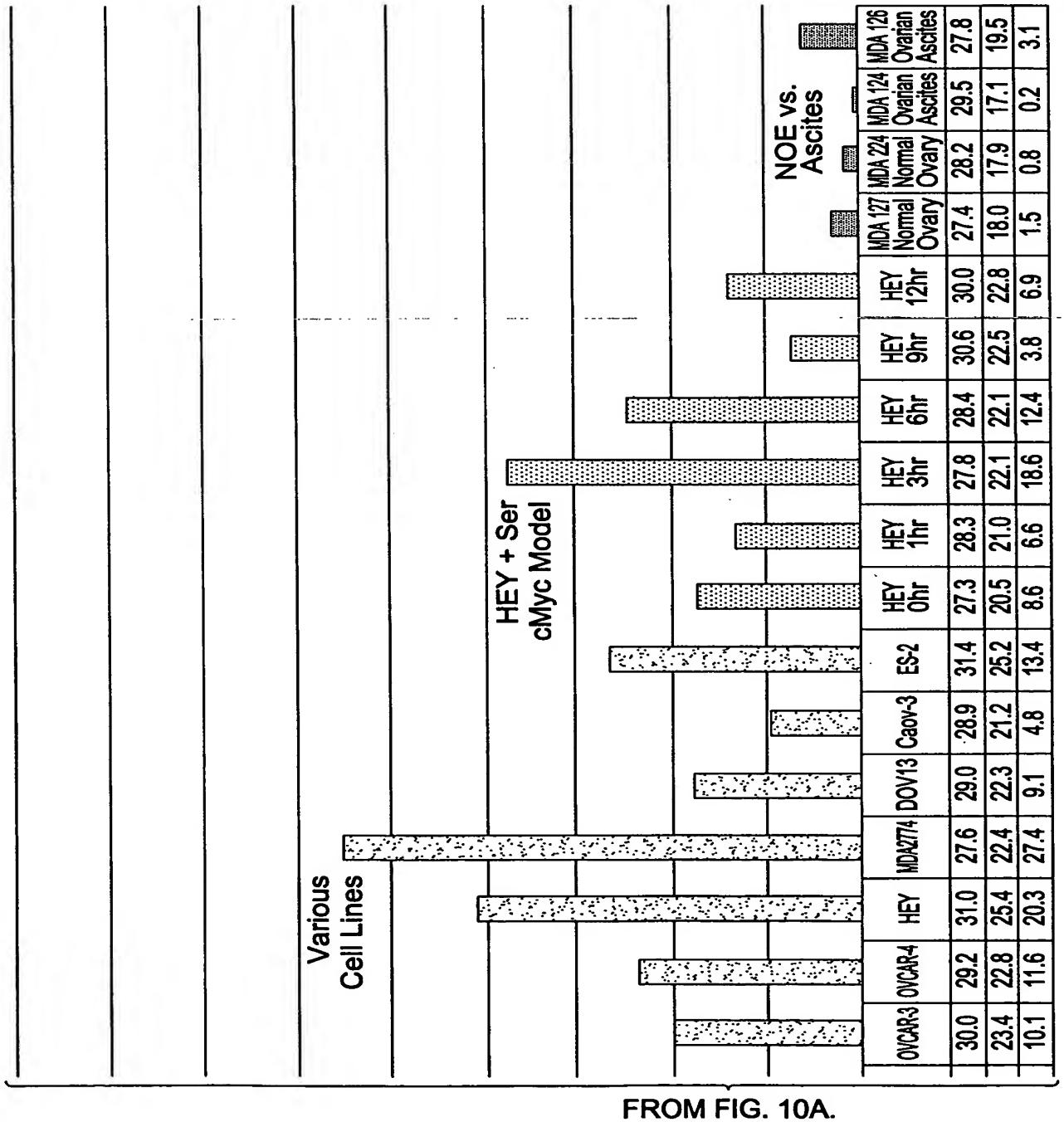


FIG. 10B.



FROM FIG. 10A.